

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: TANZI, RUDOLPH
WASCO, WILMA
 - (ii) TITLE OF INVENTION: Genetic Alterations Related To Familial
Alzheimer's Disease
 - (iii) NUMBER OF SEQUENCES: 32
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 - (B) STREET: 1100 NEW YORK AVENUE, SUITE 600
 - (C) CITY: WASHINGTON
 - (D) STATE: DC
 - (E) COUNTRY: USA
 - (F) ZIP: 20005-3934
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: To be assigned
 - (B) FILING DATE: Herewith
 - (C) CLASSIFICATION:
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/706,344
 - (B) FILING DATE: 30-AUG-1996
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 60/003,054
 - (B) FILING DATE: 31-AUG-1995
 - (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: KIM, JUDITH U.
 - (B) REGISTRATION NUMBER: 40,679
 - (C) REFERENCE/DOCKET NUMBER: 0609.4180002
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 202-371-2600
 - (B) TELEFAX: 202-371-2540
- (2) INFORMATION FOR SEQ ID NO: 1:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2765 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 249..1649

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

TGGGACAGGC AGCTCCGGGG TCCGCGGTTT CACATCGGAA ACAAACAGC GGCTGGTCTG	60
GAAGGAACCT GAGCTACGAG CCGCGGCGGC AGCGGGGCGG CGGGGAAGCG TATACCTAAT	120
CTGGGAGCCT GCAAGTGACA ACAGCCTTTG CGGTCCTTAG ACAGCTTGGC CTGGAGGAGA	180
ACACATGAAA GAAAGAACCT CAAGAGGCTT TGTTTTCTGT GAAACAGTAT TTCTATACAG	240
TTGCTCCA ATG ACA GAG TTA CCT GCA CCG TTG TCC TAC TTC CAG AAT GCA	290
Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala	
1 5 10	
CAG ATG TCT GAG GAC AAC CAC CTG AGC AAT ACT GTA CGT AGC CAG AAT	338
Gln Met Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn	
15 20 25 30	
GAC AAT AGA GAA CGG CAG GAG CAC AAC GAC AGA CGG AGC CTT GGC CAC	386
Asp Asn Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His	
35 40 45	
CCT GAG CCA TTA TCT AAT GGA CGA CCC CAG GGT AAC TCC CGG CAG GTG	434
Pro Glu Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val	
50 55 60	
GTG GAG CAA GAT GAG GAA GAA GAT GAG GAG CTG ACA TTG AAA TAT GGC	482
Val Glu Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly	
65 70 75	
GCC AAG CAT GTG ATC ATG CTC TTT GTC CCT GTG ACT CTC TGC ATG GTG	530
Ala Lys His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val	
80 85 90	
GTG GTC GTG GCT ACC ATT AAG TCA GTC AGC TTT TAT ACC CGG AAG GAT	578
Val Val Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp	
95 100 105 110	
GGG CAG CTA ATC TAT ACC CCA TTC ACA GAA GAT ACC GAG ACT GTG GGC	626
Gly Gln Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly	
115 120 125	
CAG AGA GCC CTG CAC TCA ATT CTG AAT GCT GCC ATC ATG ATC AGT GTC	674
Gln Arg Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val	
130 135 140	
ATT GTT GTC ATG ACT ATC CTC CTG GTG GTT CTG TAT AAA TAC AGG TGC	722
Ile Val Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys	
145 150 155	
TAT AAG GTC ATC CAT GCC TGG CTT ATT ATA TCA TCT CTA TTG TTG CTG	770
Tyr Lys Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Leu	
160 165 170	
TTC TTT TTT TCA TTC ATT TAC TTG GGG GAA GTG TTT AAA ACC TAT AAC	818
Phe Phe Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn	
175 180 185 190	
GTT GCT GTG GAC TAC ATT ACT GTT GCA CTC CTG ATC TGG AAT TTT GGT	866
Val Ala Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Phe Gly	
195 200 205	

GTG GTG GGA ATG ATT TCC ATT CAC TGG AAA GGT CCA CTT CGA CTC CAG Val Val Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln 210 215 220	914
CAG GCA TAT CTC ATT ATG ATT AGT GCC CTC ATG GCC CTG GTG TTT ATC Gln Ala Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile 225 230 235	962
AAG TAC CTC CCT GAA TGG ACT GCG TGG CTC ATC TTG GCT GTG ATT TCA Lys Tyr Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser 240 245 250	1010
GTA TAT GAT TTA GTG GCT GTT TTG TGT CCG AAA GGT CCA CTT CGT ATG Val Tyr Asp Leu Val Ala Val Leu Cys Pro Lys Gly Pro Leu Arg Met 255 260 265 270	1058
CTG GTT GAA ACA GCT CAG GAG AGA AAT GAA ACG CTT TTT CCA GCT CTC Leu Val Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu 275 280 285	1106
ATT TAC TCC TCA ACA ATG GTG TGG TTG GTG AAT ATG GCA GAA GGA GAC Ile Tyr Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp 290 295 300	1154
CCG GAA GCT CAA AGG AGA GTA TCC AAA AAT TCC AAG CAT AAT GCA GAA Pro Glu Ala Gln Arg Arg Val Ser Lys Asn Ser Lys His Asn Ala Glu 305 310 315	1202
AGC ACA GAA AGG GAG TCA CAA GAC ACT GTT GCA GAG AAT GAT GAT GGC Ser Thr Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly 320 325 330	1250
GGG TTC AGT GAG GAA TGG GAA GCC CAG AGG GAC AGT CAT CTA GGG CCT Gly Phe Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro 335 340 345 350	1298
CAT CGC TCT ACA CCT GAG TCA CGA GCT GCT GTC CAG GAA CTT TCC AGC His Arg Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser 355 360 365	1346
AGT ATC CTC GCT GGT GAA GAC CCA GAG GAA AGG GGA GTA AAA CTT GGA Ser Ile Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly 370 375 380	1394
TTG GGA GAT TTC ATT TTC TAC AGT GTT CTG GTT GGT AAA GCC TCA GCA Leu Gly Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala 385 390 395	1442
ACA GCC AGT GGA GAC TGG AAC ACA ACC ATA GCC TGT TTC GTA GCC ATA Thr Ala Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile 400 405 410	1490
TTA ATT GGT TTG TGC CTT ACA TTA TTA CTC CTT GCC ATT TTC AAG AAA Leu Ile Gly Leu Cys Leu Thr Leu Leu Leu Ala Ile Phe Lys Lys 415 420 425 430	1538
GCA TTG CCA GCT CTT CCA ATC TCC ATC ACC TTT GGG CTT GTT TTC TAC Ala Leu Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr 435 440 445	1586
TTT GCC ACA GAT TAT CTT GTA CAG CCT TTT ATG GAC CAA TTA GCA TTC Phe Ala Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe 445 450 455	1634

450	455	460	
CAT CAA TTT TAT ATC TAGCATATTT GCGGTTAGAA TCCCATGGAT GTTTCTTCTT			1689
His Gln Phe Tyr Ile			
465			
TGACTATAAC CAAATCTGGG GAGGACAAAG GTGATTTTCC TGTGTCCACA TCTAACAAAG			1749
TCAAGATTCC CGGCTGGACT TTTGCAGCTT CCTTCCAAGT CTTCTGACC ACCTTGCACT			1809
ATTGGACTTT GGAAGGAGGT GCCTATAGAA AACGATTTTG AACATACTTC ATCGCAGTGG			1869
ACTGTGTCCC TCGGTGCAGA AACTACCAGA TTTGAGGGAC GAGGTCAAGG AGATATGATA			1929
GGCCCGGAAG TTGCTGTGCC CCATCAGCAG CTTGACGCGT GGTCACAGGA CGATTTCCT			1989
GACACTGCGA ACTCTCAGGA CTACCGGTTA CCAAGAGGTT AGGTGAAGTG GTTTAAACCA			2049
AACGGAAGTC TTCATCTTAA ACTACACGTT GAAAATCAAC CCAATAATTC TGTATTAAC			2109
GAATTCTGAA CTTTTCAGGA GGTACTGTGA GGAAGAGCAG GCACCAGCAG CAGAATGGGG			2169
AATGGAGAGG TGGGCAGGGG TTCCAGCTTC CCTTTGATTT TTTGCTGCAG ACTCATCCTT			2229
TTTAAATGAG ACTTGTTTTT CCCTCTCTTT GAGTCAAGTC AAATATGTAG ATTGCCTTTG			2289
GCAATTCTTC TTCTCAAGCA CTGACACTCA TTACCGTCTG TGATTGCCAT TTCTTCCCAA			2349
GGCCAGTCTG AACCTGAGGT TGCTTTATCC TAAAAGTTTT AACCTCAGGT TCCAAATTCA			2409
GTAAATTTTG GAAACAGTAC AGCTATTTCT CATCAATTCT CTATCATGTT GAAGTCAAAT			2469
TTGGATTTTC CACCAAATTC TGAATTTGTA GACATACTTG TACGCTCACT TGCCCCCAGA			2529
TGCCTCCTCT GTCCTCATTC TTCTCTCCCA CACAAGCAGT CTTTTTCTAC AGCCAGTAAG			2589
GCAGCTCTGT CRTGGTAGCA GATGGTCCCA TTATTCTAGG GTCTTACTCT TTGTATGATG			2649
AAAAGAATGT GTTATGAATC GGTGCTGTCA GCCCTGCTGT CAGACCTTCT TCCACAGCAA			2709
ATGAGATGTA TGCCCAAAGC GGTAAGAATTA AAGAAGAGTA AAATGGCTGT TGAAGC			2765

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 467 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met	Thr	Glu	Leu	Pro	Ala	Pro	Leu	Ser	Tyr	Phe	Gln	Asn	Ala	Gln	Met
1				5					10					15	
Ser	Glu	Asp	Asn	His	Leu	Ser	Asn	Thr	Val	Arg	Ser	Gln	Asn	Asp	Asn
			20					25					30		
Arg	Glu	Arg	Gln	Glu	His	Asn	Asp	Arg	Arg	Ser	Leu	Gly	His	Pro	Glu
		35					40					45			

Pro	Leu	Ser	Asn	Gly	Arg	Pro	Gln	Gly	Asn	Ser	Arg	Gln	Val	Val	Glu
50						55					60				
Gln	Asp	Glu	Glu	Glu	Asp	Glu	Glu	Leu	Thr	Leu	Lys	Tyr	Gly	Ala	Lys
65					70					75					80
His	Val	Ile	Met	Leu	Phe	Val	Pro	Val	Thr	Leu	Cys	Met	Val	Val	Val
				85					90					95	
Val	Ala	Thr	Ile	Lys	Ser	Val	Ser	Phe	Tyr	Thr	Arg	Lys	Asp	Gly	Gln
			100					105					110		
Leu	Ile	Tyr	Thr	Pro	Phe	Thr	Glu	Asp	Thr	Glu	Thr	Val	Gly	Gln	Arg
		115					120					125			
Ala	Leu	His	Ser	Ile	Leu	Asn	Ala	Ala	Ile	Met	Ile	Ser	Val	Ile	Val
	130					135					140				
Val	Met	Thr	Ile	Leu	Leu	Val	Val	Leu	Tyr	Lys	Tyr	Arg	Cys	Tyr	Lys
145					150					155					160
Val	Ile	His	Ala	Trp	Leu	Ile	Ile	Ser	Ser	Leu	Leu	Leu	Leu	Phe	Phe
				165					170					175	
Phe	Ser	Phe	Ile	Tyr	Leu	Gly	Glu	Val	Phe	Lys	Thr	Tyr	Asn	Val	Ala
			180					185					190		
Val	Asp	Tyr	Ile	Thr	Val	Ala	Leu	Leu	Ile	Trp	Asn	Phe	Gly	Val	Val
		195					200					205			
Gly	Met	Ile	Ser	Ile	His	Trp	Lys	Gly	Pro	Leu	Arg	Leu	Gln	Gln	Ala
	210					215					220				
Tyr	Leu	Ile	Met	Ile	Ser	Ala	Leu	Met	Ala	Leu	Val	Phe	Ile	Lys	Tyr
225					230					235					240
Leu	Pro	Glu	Trp	Thr	Ala	Trp	Leu	Ile	Leu	Ala	Val	Ile	Ser	Val	Tyr
				245					250					255	
Asp	Leu	Val	Ala	Val	Leu	Cys	Pro	Lys	Gly	Pro	Leu	Arg	Met	Leu	Val
			260					265					270		
Glu	Thr	Ala	Gln	Glu	Arg	Asn	Glu	Thr	Leu	Phe	Pro	Ala	Leu	Ile	Tyr
		275					280					285			
Ser	Ser	Thr	Met	Val	Trp	Leu	Val	Asn	Met	Ala	Glu	Gly	Asp	Pro	Glu
		290				295					300				
Ala	Gln	Arg	Arg	Val	Ser	Lys	Asn	Ser	Lys	His	Asn	Ala	Glu	Ser	Thr
305					310					315					320
Glu	Arg	Glu	Ser	Gln	Asp	Thr	Val	Ala	Glu	Asn	Asp	Asp	Gly	Gly	Phe
				325					330					335	
Ser	Glu	Glu	Trp	Glu	Ala	Gln	Arg	Asp	Ser	His	Leu	Gly	Pro	His	Arg
			340					345					350		
Ser	Thr	Pro	Glu	Ser	Arg	Ala	Ala	Val	Gln	Glu	Leu	Ser	Ser	Ser	Ile
		355					360					365			
Leu	Ala	Gly	Glu	Asp	Pro	Glu	Glu	Arg	Gly	Val	Lys	Leu	Gly	Leu	Gly
	370					375					380				

Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala
385 390 395 400

Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile
405 410 415

Gly Leu Cys Leu Thr Leu Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu
420 425 430

Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala
435 440 445

Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln
450 455 460

Phe Tyr Ile
465

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2765 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 249..1649

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TGGGACAGGC AGCTCCGGGG TCCGCGGTTT CACATCGGAA ACAAACAGC GGCTGGTCTG	60
GAAGGAACCT GAGCTACGAG CCGCGGCGGC AGCGGGGCGG CGGGGAAGCG TATACCTAAT	120
CTGGGAGCCT GCAAGTGACA ACAGCCTTTG CGGTCCTTAG ACAGCTTGGC CTGGAGGAGA	180
ACACATGAAA GAAAGAACCT CAAGAGGCTT TGTTTTCTGT GAAACAGTAT TTCTATACAG	240
TTGCTCCA ATG ACA GAG TTA CCT GCA CCG TTG TCC TAC TTC CAG AAT GCA	290
Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala	
1 5 10	
CAG ATG TCT GAG GAC AAC CAC CTG AGC AAT ACT GTA CGT AGC CAG AAT	338
Gln Met Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn	
15 20 25 30	
GAC AAT AGA GAA CGG CAG GAG CAC AAC GAC AGA CGG AGC CTT GGC CAC	386
Asp Asn Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His	
35 40 45	
CCT GAG CCA TTA TCT AAT GGA CGA CCC CAG GGT AAC TCC CGG CAG GTG	434
Pro Glu Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val	
50 55 60	
GTG GAG CAA GAT GAG GAA GAA GAT GAG GAG CTG ACA TTG AAA TAT GGC	482
Val Glu Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly	

65	70	75	
GCC AAG CAT GTG ATC ATG CTC TTT GTC CCT GTG ACT CTC TGC ATG GTG Ala Lys His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val 80 85 90			530
GTG GTC GTG GCT ACC ATT AAG TCA GTC AGC TTT TAT ACC CGG AAG GAT Val Val Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp 95 100 105 110			578
GGG CAG CTA ATC TAT ACC CCA TTC ACA GAA GAT ACC GAG ACT GTG GGC Gly Gln Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly 115 120 125			626
CAG AGA GCC CTG CAC TCA ATT CTG AAT GCT GCC ATC ATG ATC AGT GTC Gln Arg Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val 130 135 140			674
ATT GTT GTC ATG ACT ATC CTC CTG GTG GTT CTG TAT AAA TAC AGG TGC Ile Val Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys 145 150 155			722
TAT AAG GTC ATC CAT GCC TGG CTT ATT ATA TCA TCT CTA TTG TTG CTG Tyr Lys Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Leu 160 165 170			770
TTC TTT TTT TCA TTC ATT TAC TTG GGG GAA GTG TTT AAA ACC TAT AAC Phe Phe Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn 175 180 185 190			818
GTT GCT GTG GAC TAC ATT ACT GTT GCA CTC CTG ATC TGG AAT TTT GGT Val Ala Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Phe Gly 195 200 205			866
GTG GTG GGA ATG ATT TCC ATT CAC TGG AAA GGT CCA CTT CGA CTC CAG Val Val Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln 210 215 220			914
CAG GCA TAT CTC ATT ATG ATT AGT GCC CTC ATG GCC CTG GTG TTT ATC Gln Ala Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile 225 230 235			962
AAG TAC CTC CCT GAA TGG ACT GCG TGG CTC ATC TTG GCT GTG ATT TCA Lys Tyr Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser 240 245 250			1010
GTA TAT GAT TTA GTG GCT GTT TTG CGT CTG AAA GGT CCA CTT CAT ATG Val Tyr Asp Leu Val Ala Val Leu Arg Leu Lys Gly Pro Leu His Met 255 260 265 270			1058
CTG GTT GAA ACA GCT CAG GAG AGA AAT GAA ACG CTT TTT CCA GCT CTC Leu Val Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu 275 280 285			1106
ATT TAC TCC TCA ACA ATG GTG TGG TTG GTG AAT ATG GCA GAA GGA GAC Ile Tyr Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp 290 295 300			1154
CCG GAA GCT CAA AGG AGA GTA TCC AAA AAT TCC AAG CAT AAT GCA GAA Pro Glu Ala Gln Arg Arg Val Ser Lys Asn Ser Lys His Asn Ala Glu 305 310 315			1202

AGC	ACA	GAA	AGG	GAG	TCA	CAA	GAC	ACT	GTT	GCA	GAG	AAT	GAT	GAT	GGC	1250
Ser	Thr	Glu	Arg	Glu	Ser	Gln	Asp	Thr	Val	Ala	Glu	Asn	Asp	Asp	Gly	
	320					325					330					
GGG	TTC	AGT	GAG	GAA	TGG	GAA	GCC	CAG	AGG	GAC	AGT	CAT	CTA	GGG	CCT	1298
Gly	Phe	Ser	Glu	Glu	Trp	Glu	Ala	Gln	Arg	Asp	Ser	His	Leu	Gly	Pro	
	335				340					345					350	
CAT	CGC	TCT	ACA	CCT	GAG	TCA	CGA	GCT	GCT	GTC	CAG	GAA	CTT	TCC	AGC	1346
His	Arg	Ser	Thr	Pro	Glu	Ser	Arg	Ala	Ala	Val	Gln	Glu	Leu	Ser	Ser	
				355						360					365	
AGT	ATC	CTC	GCT	GGT	GAA	GAC	CCA	GAG	GAA	AGG	GGA	GTA	AAA	CTT	GGA	1394
Ser	Ile	Leu	Ala	Gly	Glu	Asp	Pro	Glu	Glu	Arg	Gly	Val	Lys	Leu	Gly	
			370					375					380			
TTG	GGA	GAT	TTC	ATT	TTC	TAC	AGT	GTT	CTG	GTT	GGT	AAA	GCC	TCA	GCA	1442
Leu	Gly	Asp	Phe	Ile	Phe	Tyr	Ser	Val	Leu	Val	Gly	Lys	Ala	Ser	Ala	
		385					390					395				
ACA	GCC	AGT	GGA	GAC	TGG	AAC	ACA	ACC	ATA	GCC	TGT	TTC	GTA	GCC	ATA	1490
Thr	Ala	Ser	Gly	Asp	Trp	Asn	Thr	Thr	Ile	Ala	Cys	Phe	Val	Ala	Ile	
	400					405					410					
TTA	ATT	GGT	TTG	TGC	CTT	ACA	TTA	TTA	CTC	CTT	GCC	ATT	TTC	AAG	AAA	1538
Leu	Ile	Gly	Leu	Cys	Leu	Thr	Leu	Leu	Leu	Leu	Ala	Ile	Phe	Lys	Lys	
	415				420					425					430	
GCA	TTG	CCA	GCT	CTT	CCA	ATC	TCC	ATC	ACC	TTT	GGG	CTT	GTT	TTC	TAC	1586
Ala	Leu	Pro	Ala	Leu	Pro	Ile	Ser	Ile	Thr	Phe	Gly	Leu	Val	Phe	Tyr	
				435					440					445		
TTT	GCC	ACA	GAT	TAT	CTT	GTA	CAG	CCT	TTT	ATG	GAC	CAA	TTA	GCA	TTC	1634
Phe	Ala	Thr	Asp	Tyr	Leu	Val	Gln	Pro	Phe	Met	Asp	Gln	Leu	Ala	Phe	
			450					455					460			
CAT	CAA	TTT	TAT	ATC	TAGCATATTT	GCGGTTAGAA	TCCCATGGAT	GTTTCTTCTT								1689
His	Gln	Phe	Tyr	Ile												
		465														
TGACTATAAC	CAAATCTGGG	GAGGACAAAG	GTGATTTTCC	TGTGTCCACA	TCTAACAAAG											1749
TCAAGATTCC	CGGCTGGACT	TTTGCACTT	CCTTCCAAGT	CTTCCTGACC	ACCTTGCACT											1809
ATTGGACTTT	GGAAGGAGGT	GCCTATAGAA	AACGATTTTG	AACATACTTC	ATCGCAGTGG											1869
ACTGTGTCCC	TCGGTGCAGA	AACTACCAGA	TTTGAGGGAC	GAGGTCAAGG	AGATATGATA											1929
GGCCCCGAAG	TTGCTGTGCC	CCATCAGCAG	CTTGACGCGT	GGTCACAGGA	CGATTTCACT											1989
GACACTGCGA	ACTCTCAGGA	CTACCGGTTA	CCAAGAGGTT	AGGTGAAGTG	GTTTAAACCA											2049
AACGGAACTC	TTCATCTTAA	ACTACACGTT	GAAAATCAAC	CCAATAATTC	TGTATTAACT											2109
GAATTCTGAA	CTTTTCAGGA	GGTACTGTGA	GGAAGAGCAG	GCACCAGCAG	CAGAATGGGG											2169
AATGGAGAGG	TGGGCAGGGG	TTCCAGCTTC	CCTTTGATTT	TTTGCTGCAG	ACTCATCCTT											2229
TTTAAATGAG	ACTTGTTTTT	CCCTCTCTTT	GAGTCAAGTC	AAATATGTAG	ATTGCCTTTG											2289
GCAATTCTTC	TTCTCAAGCA	CTGACACTCA	TTACCGTCTG	TGATTGCCAT	TTCTTCCCAA											2349

GGCCAGTCTG AACCTGAGGT TGCTTTATCC TAAAAGTTTT AACCTCAGGT TCCAAATTCA 2409
 GTAAATTTTG GAAACAGTAC AGCTATTTCT CATCAATTCT CTATCATGTT GAAGTCAAAT 2469
 TTGGATTTTC CACCAAATTC TGAATTTGTA GACATACTTG TACGCTCACT TGCCCCCAGA 2529
 TGCCTCCTCT GTCCTCATTC TTCTCTCCCA CACAAGCAGT CTTTTTCTAC AGCCAGTAAG 2589
 GCAGCTCTGT CRTGGTAGCA GATGGTCCCA TTATTCTAGG GTCTTACTCT TTGTATGATG 2649
 AAAAGAATGT GTTATGAATC GGTGCTGTCA GCCCTGCTGT CAGACCTTCT TCCACAGCAA 2709
 ATGAGATGTA TGCCCAAAGC GGTAGAATTA AAGAAGAGTA AAATGGCTGT TGAAGC 2765

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 467 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met	Thr	Glu	Leu	Pro	Ala	Pro	Leu	Ser	Tyr	Phe	Gln	Asn	Ala	Gln	Met	1	5	10	15
Ser	Glu	Asp	Asn	His	Leu	Ser	Asn	Thr	Val	Arg	Ser	Gln	Asn	Asp	Asn	20	25	30	
Arg	Glu	Arg	Gln	Glu	His	Asn	Asp	Arg	Arg	Ser	Leu	Gly	His	Pro	Glu	35	40	45	
Pro	Leu	Ser	Asn	Gly	Arg	Pro	Gln	Gly	Asn	Ser	Arg	Gln	Val	Val	Glu	50	55	60	
Gln	Asp	Glu	Glu	Glu	Asp	Glu	Glu	Leu	Thr	Leu	Lys	Tyr	Gly	Ala	Lys	65	70	75	80
His	Val	Ile	Met	Leu	Phe	Val	Pro	Val	Thr	Leu	Cys	Met	Val	Val	Val	85	90	95	
Val	Ala	Thr	Ile	Lys	Ser	Val	Ser	Phe	Tyr	Thr	Arg	Lys	Asp	Gly	Gln	100	105	110	
Leu	Ile	Tyr	Thr	Pro	Phe	Thr	Glu	Asp	Thr	Glu	Thr	Val	Gly	Gln	Arg	115	120	125	
Ala	Leu	His	Ser	Ile	Leu	Asn	Ala	Ala	Ile	Met	Ile	Ser	Val	Ile	Val	130	135	140	
Val	Met	Thr	Ile	Leu	Leu	Val	Val	Leu	Tyr	Lys	Tyr	Arg	Cys	Tyr	Lys	145	150	155	160
Val	Ile	His	Ala	Trp	Leu	Ile	Ile	Ser	Ser	Leu	Leu	Leu	Leu	Phe	Phe	165	170	175	
Phe	Ser	Phe	Ile	Tyr	Leu	Gly	Glu	Val	Phe	Lys	Thr	Tyr	Asn	Val	Ala	180	185	190	
Val	Asp	Tyr	Ile	Thr	Val	Ala	Leu	Leu	Ile	Trp	Asn	Phe	Gly	Val	Val				

195	200	205
Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala 210 215 220		
Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr 225 230 235 240		
Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr 245 250 255		
Asp Leu Val Ala Val Leu Arg Leu Lys Gly Pro Leu His Met Leu Val 260 265 270		
Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr 275 280 285		
Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu 290 295 300		
Ala Gln Arg Arg Val Ser Lys Asn Ser Lys His Asn Ala Glu Ser Thr 305 310 315 320		
Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly Gly Phe 325 330 335		
Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg 340 345 350		
Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser Ser Ile 355 360 365		
Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly 370 375 380		
Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala 385 390 395 400		
Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile 405 410 415		
Gly Leu Cys Leu Thr Leu Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu 420 425 430		
Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala 435 440 445		
Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln 450 455 460		
Phe Tyr Ile 465		

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CACCCATTTA CAAGTTTAGC

20

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GATGAGACAA GTGCCGTGAA

20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gly Gln Ala Ala Pro Gly Ser Ala Val Ser His Arg Lys Gln Asn Ser
1 5 10 15

Gly Trp Ser Gly Arg Asn Leu Ser Tyr Glu Pro Arg Arg Gln Arg Gly
20 25 30

Gly Gly Glu Ala Tyr Thr
35

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ser Gly Ser Leu Gln Val Thr Thr Ala Phe Ala Val Leu Arg Gln Leu
1 5 10 15

Gly Leu Glu Glu Asn Thr
20

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Lys Lys Glu Pro Gln Glu Ala Leu Phe Ser Val Lys Gln Tyr Phe Tyr
1 5 10 15

Thr Val Ala Pro
20

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

His Ile Cys Gly
1

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Asn Pro Met Asp Val Ser Ser Leu Thr Ile Thr Lys Ser Gly Glu Asp
1 5 10 15

Lys Gly Asp Phe Pro Val Ser Thr Ser Asn Lys Val Lys Ile Pro Gly
 20 25 30
 Trp Thr Phe Ala Ala Ser Phe Gln Val Phe Leu Thr Thr Leu His Tyr
 35 40 45
 Trp Thr Leu Glu Gly Gly Ala Tyr Arg Lys Arg Phe
 50 55 60

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Thr Tyr Phe Ile Ala Val Asp Cys Val Pro Arg Cys Arg Asn Tyr Gln
 1 5 10 15
 Ile

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Gly Thr Arg Ser Arg Arg Tyr Asp Arg Pro Gly Ser Cys Cys Ala Pro
 1 5 10 15
 Ser Ala Ala

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Arg Val Val Thr Gly Arg Phe His
1 5

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

His Cys Glu Leu Ser Gly Leu Pro Val Thr Lys Arg Leu Gly Glu Val
1 5 10 15
Val

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Thr Lys Arg Asn Ser Ser Ser
1 5

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Lys Ser Thr Gln
1

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Phe Cys Ile Asn
1

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Ile Leu Asn Phe Ser Gly Gly Thr Val Arg Lys Ser Arg His Gln Gln
1 5 10 15

Gln Asn Gly Glu Trp Arg Gly Gly Gln Gly Phe Gln Leu Pro Phe Asp
20 25 30

Phe Leu Leu Gln Thr His Pro Phe
35 40

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Arg Leu Val Phe Pro Ser Leu
1 5

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Val Lys Ser Asn Met
1 5

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Ile Ala Phe Gly Asn Ser Ser Ser Gln Ala Leu Thr Leu Ile Thr Val
1 5 10 15

Cys Asp Cys His Phe Phe Pro Arg Pro Val
20 25

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Gly Cys Phe Ile Leu Lys Val Leu Thr Ser Gly Ser Lys Phe Ser Lys
1 5 10 15

Phe Trp Lys Gln Tyr Ser Tyr Phe Ser Ser Ile Leu Tyr His Val Glu
20 25 30

Val Lys Phe Gly Phe Ser Thr Lys Phe
35 40

(2) INFORMATION FOR SEQ ID NO:24:

(ii) MOLECULE TYPE: peptide

Ile	Cys	Arg	His	Thr	Cys	Thr	Leu	Thr	Cys	Pro	Gln	Met	Pro	Pro	Leu
1				5					10					15	
Ser	Ser	Phe	Phe	Ser	Pro	Thr	Gln	Ala	Val	Phe	Phe	Tyr	Ser	Gln	
			20					25					30		

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

Gly Ser Ser Val Xaa Val Ala Asp Gly Pro Ile Ile Leu Gly Ser Tyr
1 5 10 15
Ser Leu Tyr Asp Glu Lys Asn Val Leu
20 25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

Ile Gly Ala Val Ser Pro Ala Val Arg Pro Ser Ser Thr Ala Asn Glu
1 5 10 15
Met Tyr Ala Gln Ser Gly Arg Ile Lys Glu Glu
20 25

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2765 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION:249..1649

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

TGGGACAGGC AGCTCCGGGG TCCGCGGTTT CACATCGGAA ACAAACAGC GGCTGGTCTG	60
GAAGGAACCT GAGCTACGAG CCGCGGCGGC AGCGGGGCGG CGGGGAAGCG TATACCTAAT	120
CTGGGAGCCT GCAAGTGACA ACAGCCTTTG CGGTCCTTAG ACAGCTTGGC CTGGAGGAGA	180
ACACATGAAA GAAAGAACCT CAAGAGGCTT TGTTTTCTGT GAAACAGTAT TTCTATACAG	240
TTGCTCCA ATG ACA GAG TTA CCT GCA CCG TTG TCC TAC TTC CAG AAT GCA	290
Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala	
1 5 10	
CAG ATG TCT GAG GAC AAC CAC CTG AGC AAT ACT GTA CGT AGC CAG AAT	338
Gln Met Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn	
15 20 25 30	
GAC AAT AGA GAA CGG CAG GAG CAC AAC GAC AGA CGG AGC CTT GGC CAC	386
Asp Asn Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His	
35 40 45	
CCT GAG CCA TTA TCT AAT GGA CGA CCC CAG GGT AAC TCC CGG CAG GTG	434
Pro Glu Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val	
50 55 60	
GTG GAG CAA GAT GAG GAA GAA GAT GAG GAG CTG ACA TTG AAA TAT GGC	482
Val Glu Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly	
65 70 75	
GCC AAG CAT GTG ATC ATG CTC TTT GTC CCT GTG ACT CTC TGC ATG GTG	530
Ala Lys His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val	
80 85 90	
GTG GTC GTG GCT ACC ATT AAG TCA GTC AGC TTT TAT ACC CGG AAG GAT	578
Val Val Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp	
95 100 105 110	
GGG CAG CTA ATC TAT ACC CCA TTC ACA GAA GAT ACC GAG ACT GTG GGC	626
Gly Gln Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly	
115 120 125	
CAG AGA GCC CTG CAC TCA ATT CTG AAT GCT GCC ATC ATG ATC AGT GTC	674
Gln Arg Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val	
130 135 140	
ATT GTT GTC ATG ACT ATC CTC CTG GTG GTT CTG TAT AAA TAC AGG TGC	722

Ile	Val	Val	Met	Thr	Ile	Leu	Leu	Val	Val	Leu	Tyr	Lys	Tyr	Arg	Cys	
		145					150					155				
TAT	AAG	GTC	ATC	CAT	GCC	TGG	CTT	ATT	ATA	TCA	TCT	CTA	TTG	TTG	CTG	770
Tyr	Lys	Val	Ile	His	Ala	Trp	Leu	Ile	Ile	Ser	Ser	Leu	Leu	Leu	Leu	
	160					165					170					
TTC	TTT	TTT	TCA	TTC	ATT	TAC	TTG	GGG	GAA	GTG	TTT	AAA	ACC	TAT	AAC	818
Phe	Phe	Phe	Ser	Phe	Ile	Tyr	Leu	Gly	Glu	Val	Phe	Lys	Thr	Tyr	Asn	
175					180					185					190	
GTT	GCT	GTG	GAC	TAC	ATT	ACT	GTT	GCA	CTC	CTG	ATC	TGG	AAT	TTT	GGT	866
Val	Ala	Val	Asp	Tyr	Ile	Thr	Val	Ala	Leu	Leu	Ile	Trp	Asn	Phe	Gly	
				195					200					205		
GTG	GTG	GGA	ATG	ATT	TCC	ATT	CAC	TGG	AAA	GGT	CCA	CTT	CGA	CTC	CAG	914
Val	Val	Gly	Met	Ile	Ser	Ile	His	Trp	Lys	Gly	Pro	Leu	Arg	Leu	Gln	
			210					215					220			
CAG	GCA	TAT	CTC	ATT	ATG	ATT	AGT	GCC	CTC	ATG	GCC	CTG	GTG	TTT	ATC	962
Gln	Ala	Tyr	Leu	Ile	Met	Ile	Ser	Ala	Leu	Met	Ala	Leu	Val	Phe	Ile	
		225					230					235				
AAG	TAC	CTC	CCT	GAA	TGG	ACT	GCG	TGG	CTC	ATC	TTG	GCT	GTG	ATT	TCA	1010
Lys	Tyr	Leu	Pro	Glu	Trp	Thr	Ala	Trp	Leu	Ile	Leu	Ala	Val	Ile	Ser	
	240					245					250					
GTA	TAT	GAT	TTA	GTG	GCT	GTT	TTG	CGT	CCG	AAA	GGT	CCA	CTT	CGT	ATG	1058
Val	Tyr	Asp	Leu	Val	Ala	Val	Leu	Arg	Pro	Lys	Gly	Pro	Leu	Arg	Met	
255					260					265					270	
CTG	GTT	GAA	ACA	GCT	CAG	GAG	AGA	AAT	GAA	ACG	CTT	TTT	CCA	GCT	CTC	1106
Leu	Val	Glu	Thr	Ala	Gln	Glu	Arg	Asn	Glu	Thr	Leu	Phe	Pro	Ala	Leu	
				275					280					285		
ATT	TAC	TCC	TCA	ACA	ATG	GTG	TGG	TTG	GTG	AAT	ATG	GCA	GAA	GGA	GAC	1154
Ile	Tyr	Ser	Ser	Thr	Met	Val	Trp	Leu	Val	Asn	Met	Ala	Glu	Gly	Asp	
			290					295					300			
CCG	GAA	GCT	CAA	AGG	AGA	GTA	TCC	AAA	AAT	TCC	AAG	CAT	AAT	GCA	GAA	1202
Pro	Glu	Ala	Gln	Arg	Arg	Val	Ser	Lys	Asn	Ser	Lys	His	Asn	Ala	Glu	
		305					310					315				
AGC	ACA	GAA	AGG	GAG	TCA	CAA	GAC	ACT	GTT	GCA	GAG	AAT	GAT	GAT	GGC	1250
Ser	Thr	Glu	Arg	Glu	Ser	Gln	Asp	Thr	Val	Ala	Glu	Asn	Asp	Asp	Gly	
	320					325					330					
GGG	TTC	AGT	GAG	GAA	TGG	GAA	GCC	CAG	AGG	GAC	AGT	CAT	CTA	GGG	CCT	1298
Gly	Phe	Ser	Glu	Glu	Trp	Glu	Ala	Gln	Arg	Asp	Ser	His	Leu	Gly	Pro	
335					340					345					350	
CAT	CGC	TCT	ACA	CCT	GAG	TCA	CGA	GCT	GCT	GTC	CAG	GAA	CTT	TCC	AGC	1346
His	Arg	Ser	Thr	Pro	Glu	Ser	Arg	Ala	Ala	Val	Gln	Glu	Leu	Ser	Ser	
				355					360					365		
AGT	ATC	CTC	GCT	GGT	GAA	GAC	CCA	GAG	GAA	AGG	GGA	GTA	AAA	CTT	GGA	1394
Ser	Ile	Leu	Ala	Gly	Glu	Asp	Pro	Glu	Glu	Arg	Gly	Val	Lys	Leu	Gly	
			370					375					380			
TTG	GGA	GAT	TTC	ATT	TTC	TAC	AGT	GTT	CTG	GTT	GGT	AAA	GCC	TCA	GCA	1442
Leu	Gly	Asp	Phe	Ile	Phe	Tyr	Ser	Val	Leu	Val	Gly	Lys	Ala	Ser	Ala	
		385					390					395				

ACA GCC AGT GGA GAC TGG AAC ACA ACC ATA GCC TGT TTC GTA GCC ATA	1490
Thr Ala Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile	
400 405 410	
TTA ATT GGT TTG TGC CTT ACA TTA TTA CTC CTT GCC ATT TTC AAG AAA	1538
Leu Ile Gly Leu Cys Leu Thr Leu Leu Leu Leu Ala Ile Phe Lys Lys	
415 420 425 430	
GCA TTG CCA GCT CTT CCA ATC TCC ATC ACC TTT GGG CTT GTT TTC TAC	1586
Ala Leu Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr	
435 440 445	
TTT GCC ACA GAT TAT CTT GTA CAG CCT TTT ATG GAC CAA TTA GCA TTC	1634
Phe Ala Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe	
450 455 460	
CAT CAA TTT TAT ATC TAGCATATTT GCGGTTAGAA TCCCATGGAT GTTCTTCTT	1689
His Gln Phe Tyr Ile	
465	
TGACTATAAC CAAATCTGGG GAGGACAAAG GTGATTTTCC TGTGTCCACA TCTAACAAAG	1749
TCAAGATTCC CGGCTGGACT TTTGCAGCTT CCTTCCAAGT CTTCTGACC ACCTTGCACT	1809
ATTGGACTTT GGAAGGAGGT GCCTATAGAA AACGATTTTG AACATACTTC ATCGCAGTGG	1869
ACTGTGTCCC TCGGTGCAGA AACTACCAGA TTTGAGGGAC GAGGTCAAGG AGATATGATA	1929
GGCCCGGAAG TTGCTGTGCC CCATCAGCAG CTTGACGCGT GGTCACAGGA CGATTTCCT	1989
GACACTGCGA ACTCTCAGGA CTACCGGTTA CCAAGAGGTT AGGTGAAGTG GTTTAAACCA	2049
AACGGAATC TTCATCTTAA ACTACACGTT GAAAATCAAC CCAATAATTC TGTATTAACT	2109
GAATTCTGAA CTTTTCAGGA GGTACTGTGA GGAAGAGCAG GCACCAGCAG CAGAATGGGG	2169
AATGGAGAGG TGGGCAGGGG TTCCAGCTTC CCTTTGATTT TTTGCTGCAG ACTCATCCTT	2229
TTTAAATGAG ACTTGTTTTT CCCTCTCTTT GAGTCAAGTC AAATATGTAG ATTGCCTTTG	2289
GCAATTCCTT TTCTCAAGCA CTGACACTCA TTACCGTCTG TGATTGCCAT TTCTTCCCAA	2349
GGCCAGTCTG AACCTGAGGT TGCTTTATCC TAAAAGTTTT AACCTCAGGT TCCAAATTCA	2409
GTAAATTTTG GAAACAGTAC AGCTATTTCT CATCAATTCT CTATCATGTT GAAGTCAAAT	2469
TTGGATTTTC CACCAAATTC TGAATTTGTA GACATACTTG TACGCTCACT TGCCCCCAGA	2529
TGCCTCCTCT GTCCTCATTC TTCTCTCCCA CACAAGCAGT CTTTTTCTAC AGCCAGTAAG	2589
GCAGCTCTGT CRTGGTAGCA GATGGTCCCA TTATTCTAGG GTCTTACTCT TTGTATGATG	2649
AAAAGAATGT GTTATGAATC GGTGCTGTCA GCCCTGCTGT CAGACCTTCT TCCACAGCAA	2709
ATGAGATGTA TGCCCCAAGC GGTAAGAATTA AAGAAGAGTA AAATGGCTGT TGAAGC	2765

(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 467 amino acids
 - (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Met	Thr	Glu	Leu	Pro	Ala	Pro	Leu	Ser	Tyr	Phe	Gln	Asn	Ala	Gln	Met	1	5	10	15
Ser	Glu	Asp	Asn	His	Leu	Ser	Asn	Thr	Val	Arg	Ser	Gln	Asn	Asp	Asn	20	25	30	
Arg	Glu	Arg	Gln	Glu	His	Asn	Asp	Arg	Arg	Ser	Leu	Gly	His	Pro	Glu	35	40	45	
Pro	Leu	Ser	Asn	Gly	Arg	Pro	Gln	Gly	Asn	Ser	Arg	Gln	Val	Val	Glu	50	55	60	
Gln	Asp	Glu	Glu	Glu	Asp	Glu	Glu	Leu	Thr	Leu	Lys	Tyr	Gly	Ala	Lys	65	70	75	80
His	Val	Ile	Met	Leu	Phe	Val	Pro	Val	Thr	Leu	Cys	Met	Val	Val	Val	85	90	95	
Val	Ala	Thr	Ile	Lys	Ser	Val	Ser	Phe	Tyr	Thr	Arg	Lys	Asp	Gly	Gln	100	105	110	
Leu	Ile	Tyr	Thr	Pro	Phe	Thr	Glu	Asp	Thr	Glu	Thr	Val	Gly	Gln	Arg	115	120	125	
Ala	Leu	His	Ser	Ile	Leu	Asn	Ala	Ala	Ile	Met	Ile	Ser	Val	Ile	Val	130	135	140	
Val	Met	Thr	Ile	Leu	Leu	Val	Val	Leu	Tyr	Lys	Tyr	Arg	Cys	Tyr	Lys	145	150	155	160
Val	Ile	His	Ala	Trp	Leu	Ile	Ile	Ser	Ser	Leu	Leu	Leu	Leu	Phe	Phe	165	170	175	
Phe	Ser	Phe	Ile	Tyr	Leu	Gly	Glu	Val	Phe	Lys	Thr	Tyr	Asn	Val	Ala	180	185	190	
Val	Asp	Tyr	Ile	Thr	Val	Ala	Leu	Leu	Ile	Trp	Asn	Phe	Gly	Val	Val	195	200	205	
Gly	Met	Ile	Ser	Ile	His	Trp	Lys	Gly	Pro	Leu	Arg	Leu	Gln	Gln	Ala	210	215	220	
Tyr	Leu	Ile	Met	Ile	Ser	Ala	Leu	Met	Ala	Leu	Val	Phe	Ile	Lys	Tyr	225	230	235	240
Leu	Pro	Glu	Trp	Thr	Ala	Trp	Leu	Ile	Leu	Ala	Val	Ile	Ser	Val	Tyr	245	250	255	
Asp	Leu	Val	Ala	Val	Leu	Arg	Pro	Lys	Gly	Pro	Leu	Arg	Met	Leu	Val	260	265	270	
Glu	Thr	Ala	Gln	Glu	Arg	Asn	Glu	Thr	Leu	Phe	Pro	Ala	Leu	Ile	Tyr	275	280	285	
Ser	Ser	Thr	Met	Val	Trp	Leu	Val	Asn	Met	Ala	Glu	Gly	Asp	Pro	Glu	290	295	300	

Ala Gln Arg Arg Val Ser Lys Asn Ser Lys His Asn Ala Glu Ser Thr
305 310 315 320

Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly Gly Phe
325 330 335

Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg
340 345 350

Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser Ser Ile
355 360 365

Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly
370 375 380

Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala
385 390 395 400

Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile
405 410 415

Gly Leu Cys Leu Thr Leu Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu
420 425 430

Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala
435 440 445

Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln
450 455 460

Phe Tyr Ile
465

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2765 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 249..1649

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

TGGGACAGGC AGCTCCGGGG TCCGCGGTTT CACATCGGAA ACAAACAGC GGCTGGTCTG 60

GAAGGAACCT GAGCTACGAG CCGCGGCGGC AGCGGGGCGG CGGGGAAGCG TATACCTAAT 120

CTGGGAGCCT GCAAGTGACA ACAGCCTTTG CGGTCCTTAG ACAGCTTGGC CTGGAGGAGA 180

ACACATGAAA GAAAGAACCT CAAGAGGCTT TGTTTTCTGT GAAACAGTAT TTCTATACAG 240

TTGCTCCA ATG ACA GAG TTA CCT GCA CCG TTG TCC TAC TTC CAG AAT GCA 290

Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala

1	5	10	
CAG ATG TCT GAG GAC AAC CAC CTG AGC AAT ACT GTA CGT AGC CAG AAT Gln Met Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn 15 20 25 30			338
GAC AAT AGA GAA CGG CAG GAG CAC AAC GAC AGA CGG AGC CTT GGC CAC Asp Asn Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His 35 40 45			386
CCT GAG CCA TTA TCT AAT GGA CGA CCC CAG GGT AAC TCC CGG CAG GTG Pro Glu Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val 50 55 60			434
GTG GAG CAA GAT GAG GAA GAA GAT GAG GAG CTG ACA TTG AAA TAT GGC Val Glu Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly 65 70 75			482
GCC AAG CAT GTG ATC ATG CTC TTT GTC CCT GTG ACT CTC TGC ATG GTG Ala Lys His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val 80 85 90			530
GTG GTC GTG GCT ACC ATT AAG TCA GTC AGC TTT TAT ACC CGG AAG GAT Val Val Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp 95 100 105 110			578
GGG CAG CTA ATC TAT ACC CCA TTC ACA GAA GAT ACC GAG ACT GTG GGC Gly Gln Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly 115 120 125			626
CAG AGA GCC CTG CAC TCA ATT CTG AAT GCT GCC ATC ATG ATC AGT GTC Gln Arg Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val 130 135 140			674
ATT GTT GTC ATG ACT ATC CTC CTG GTG GTT CTG TAT AAA TAC AGG TGC Ile Val Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys 145 150 155			722
TAT AAG GTC ATC CAT GCC TGG CTT ATT ATA TCA TCT CTA TTG TTG CTG Tyr Lys Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Leu 160 165 170			770
TTC TTT TTT TCA TTC ATT TAC TTG GGG GAA GTG TTT AAA ACC TAT AAC Phe Phe Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn 175 180 185 190			818
GTT GCT GTG GAC TAC ATT ACT GTT GCA CTC CTG ATC TGG AAT TTT GGT Val Ala Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Phe Gly 195 200 205			866
GTG GTG GGA ATG ATT TCC ATT CAC TGG AAA GGT CCA CTT CGA CTC CAG Val Val Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln 210 215 220			914
CAG GCA TAT CTC ATT ATG ATT AGT GCC CTC ATG GCC CTG GTG TTT ATC Gln Ala Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile 225 230 235			962
AAG TAC CTC CCT GAA TGG ACT GCG TGG CTC ATC TTG GCT GTG ATT TCA Lys Tyr Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser 240 245 250			1010

GTA TAT GAT TTA GTG GCT GTT TTG TGT CTG AAA GGT CCA CTT CGT ATG Val Tyr Asp Leu Val Ala Val Leu Cys Leu Lys Gly Pro Leu Arg Met 255 260 265 270	1058
CTG GTT GAA ACA GCT CAG GAG AGA AAT GAA ACG CTT TTT CCA GCT CTC Leu Val Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu 275 280 285	1106
ATT TAC TCC TCA ACA ATG GTG TGG TTG GTG AAT ATG GCA GAA GGA GAC Ile Tyr Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp 290 295 300	1154
CCG GAA GCT CAA AGG AGA GTA TCC AAA AAT TCC AAG CAT AAT GCA GAA Pro Glu Ala Gln Arg Arg Val Ser Lys Asn Ser Lys His Asn Ala Glu 305 310 315	1202
AGC ACA GAA AGG GAG TCA CAA GAC ACT GTT GCA GAG AAT GAT GAT GGC Ser Thr Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly 320 325 330	1250
GGG TTC AGT GAG GAA TGG GAA GCC CAG AGG GAC AGT CAT CTA GGG CCT Gly Phe Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro 335 340 345 350	1298
CAT CGC TCT ACA CCT GAG TCA CGA GCT GCT GTC CAG GAA CTT TCC AGC His Arg Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser 355 360 365	1346
AGT ATC CTC GCT GGT GAA GAC CCA GAG GAA AGG GGA GTA AAA CTT GGA Ser Ile Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly 370 375 380	1394
TTG GGA GAT TTC ATT TTC TAC AGT GTT CTG GTT GGT AAA GCC TCA GCA Leu Gly Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala 385 390 395	1442
ACA GCC AGT GGA GAC TGG AAC ACA ACC ATA GCC TGT TTC GTA GCC ATA Thr Ala Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile 400 405 410	1490
TTA ATT GGT TTG TGC CTT ACA TTA TTA CTC CTT GCC ATT TTC AAG AAA Leu Ile Gly Leu Cys Leu Thr Leu Leu Leu Leu Ala Ile Phe Lys Lys 415 420 425 430	1538
GCA TTG CCA GCT CTT CCA ATC TCC ATC ACC TTT GGG CTT GTT TTC TAC Ala Leu Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr 435 440 445	1586
TTT GCC ACA GAT TAT CTT GTA CAG CCT TTT ATG GAC CAA TTA GCA TTC Phe Ala Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe 450 455 460	1634
CAT CAA TTT TAT ATC TAGCATATTT GCGGTTAGAA TCCCATGGAT GTTTCTTCTT His Gln Phe Tyr Ile 465	1689
TGACTATAAC CAAATCTGGG GAGGACAAAG GTGATTTTCC TGTGTCCACA TCTAACAAAG	1749
TCAAGATTCC CGGCTGGACT TTTGAGCTT CCTTCCAAGT CTTCTGACC ACCTTGCACT	1809
ATTGGACTTT GGAAGGAGGT GCCTATAGAA AACGATTTTG AACATACTTC ATCGCAGTGG	1869


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ACTGTGTCCC TCGGTGCAGA AACTACCAGA TTTGAGGGAC GAGGTCAAGG AGATATGATA 1929
GGCCCGGAAG TTGCTGTGCC CCATCAGCAG CTTGACGCGT GGTCACAGGA CGATTTCACT 1989
GACACTGCGA ACTCTCAGGA CTACCGGTTA CCAAGAGGTT AGGTGAAGTG GTTTAAACCA 2049
AACGGAACTC TTCATCTTAA ACTACACGTT GAAAATCAAC CCAATAATTC TGTATTAAC 2109
GAATTCTGAA CTTTTCAGGA GGTACTGTGA GGAAGAGCAG GCACCAGCAG CAGAATGGGG 2169
AATGGAGAGG TGGGCAGGGG TTCCAGCTTC CCTTTGATTT TTTGCTGCAG ACTCATCCTT 2229
TTTAAATGAG ACTTGTTTTT CCCTCTCTTT GAGTCAAGTC AAATATGTAG ATTGCCTTTG 2289
GCAATTCTTC TTCTCAAGCA CTGACACTCA TTACCGTCTG TGATTGCCAT TTCTTCCCAA 2349
GGCCAGTCTG AACCTGAGGT TGCTTTATCC TAAAAGTTTT AACCTCAGGT TCCAAATTCA 2409
GTAAATTTTG GAAACAGTAC AGCTATTTCT CATCAATTCT CTATCATGTT GAAGTCAAAT 2469
TTGGATTTTC CACCAAATTC TGAATTTGTA GACATACTTG TACGCTCACT TGCCCCCAGA 2529
TGCCTCCTCT GTCCTCATTC TTCTCTCCCA CACAAGCAGT CTTTTTCTAC AGCCAGTAAG 2589
GCAGCTCTGT CRTGGTAGCA GATGGTCCCA TTATTCTAGG GTCTTACTCT TTGTATGATG 2649
AAAAGAATGT GTTATGAATC GGTGCTGTCA GCCCTGCTGT CAGACCTTCT TCCACAGCAA 2709
ATGAGATGTA TGCCCAAAGC GGTAGAATTA AAGAAGAGTA AAATGGCTGT TGAAGC 2765

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(2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 467 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

```

Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala Gln Met
 1             5             10             15
Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn Asp Asn
      20             25             30
Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His Pro Glu
      35             40             45
Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val Val Glu
      50             55             60
Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys
      65             70             75             80
His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val
      85             90             95
Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln
      100            105            110

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Leu	Ile	Tyr	Thr	Pro	Phe	Thr	Glu	Asp	Thr	Glu	Thr	Val	Gly	Gln	Arg		
		115					120					125					
Ala	Leu	His	Ser	Ile	Leu	Asn	Ala	Ala	Ile	Met	Ile	Ser	Val	Ile	Val		
	130					135					140						
Val	Met	Thr	Ile	Leu	Leu	Val	Val	Leu	Tyr	Lys	Tyr	Arg	Cys	Tyr	Lys		
145					150					155					160		
Val	Ile	His	Ala	Trp	Leu	Ile	Ile	Ser	Ser	Leu	Leu	Leu	Leu	Phe	Phe		
				165					170					175			
Phe	Ser	Phe	Ile	Tyr	Leu	Gly	Glu	Val	Phe	Lys	Thr	Tyr	Asn	Val	Ala		
			180					185					190				
Val	Asp	Tyr	Ile	Thr	Val	Ala	Leu	Leu	Ile	Trp	Asn	Phe	Gly	Val	Val		
	195						200					205					
Gly	Met	Ile	Ser	Ile	His	Trp	Lys	Gly	Pro	Leu	Arg	Leu	Gln	Gln	Ala		
	210					215					220						
Tyr	Leu	Ile	Met	Ile	Ser	Ala	Leu	Met	Ala	Leu	Val	Phe	Ile	Lys	Tyr		
225					230					235					240		
Leu	Pro	Glu	Trp	Thr	Ala	Trp	Leu	Ile	Leu	Ala	Val	Ile	Ser	Val	Tyr		
				245					250					255			
Asp	Leu	Val	Ala	Val	Leu	Cys	Leu	Lys	Gly	Pro	Leu	Arg	Met	Leu	Val		
			260					265					270				
Glu	Thr	Ala	Gln	Glu	Arg	Asn	Glu	Thr	Leu	Phe	Pro	Ala	Leu	Ile	Tyr		
		275					280					285					
Ser	Ser	Thr	Met	Val	Trp	Leu	Val	Asn	Met	Ala	Glu	Gly	Asp	Pro	Glu		
	290					295					300						
Ala	Gln	Arg	Arg	Val	Ser	Lys	Asn	Ser	Lys	His	Asn	Ala	Glu	Ser	Thr		
305					310					315					320		
Glu	Arg	Glu	Ser	Gln	Asp	Thr	Val	Ala	Glu	Asn	Asp	Asp	Gly	Gly	Phe		
				325					330					335			
Ser	Glu	Glu	Trp	Glu	Ala	Gln	Arg	Asp	Ser	His	Leu	Gly	Pro	His	Arg		
			340					345					350				
Ser	Thr	Pro	Glu	Ser	Arg	Ala	Ala	Val	Gln	Glu	Leu	Ser	Ser	Ser	Ile		
		355					360					365					
Leu	Ala	Gly	Glu	Asp	Pro	Glu	Glu	Arg	Gly	Val	Lys	Leu	Gly	Leu	Gly		
	370					375					380						
Asp	Phe	Ile	Phe	Tyr	Ser	Val	Leu	Val	Gly	Lys	Ala	Ser	Ala	Thr	Ala		
385					390					395					400		
Ser	Gly	Asp	Trp	Asn	Thr	Thr	Ile	Ala	Cys	Phe	Val	Ala	Ile	Leu	Ile		
				405					410					415			
Gly	Leu	Cys	Leu	Thr	Leu	Leu	Leu	Leu	Ala	Ile	Phe	Lys	Lys	Ala	Leu		
			420					425					430				
Pro	Ala	Leu	Pro	Ile	Ser	Ile	Thr	Phe	Gly	Leu	Val	Phe	Tyr	Phe	Ala		
		435					440					445					

Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln
450 455 460

Phe Tyr Ile
465

(2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2765 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:249..1649

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

TGGGACAGGC AGCTCCGGGG TCCGCGGTTT CACATCGGAA ACAAACAGC GGCTGGTCTG	60
GAAGGAACCT GAGCTACGAG CCGCGGCGGC AGCGGGGCGG CGGGGAAGCG TATACCTAAT	120
CTGGGAGCCT GCAAGTGACA ACAGCCTTTG CGGTCCTTAG ACAGCTTGGC CTGGAGGAGA	180
ACACATGAAA GAAAGAACCT CAAGAGGCTT TGTTTTCTGT GAAACAGTAT TTCTATACAG	240
TTGCTCCA ATG ACA GAG TTA CCT GCA CCG TTG TCC TAC TTC CAG AAT GCA	290
Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala	
1 5 10	
CAG ATG TCT GAG GAC AAC CAC CTG AGC AAT ACT GTA CGT AGC CAG AAT	338
Gln Met Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn	
15 20 25 30	
GAC AAT AGA GAA CGG CAG GAG CAC AAC GAC AGA CGG AGC CTT GGC CAC	386
Asp Asn Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His	
35 40 45	
CCT GAG CCA TTA TCT AAT GGA CGA CCC CAG GGT AAC TCC CGG CAG GTG	434
Pro Glu Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val	
50 55 60	
GTG GAG CAA GAT GAG GAA GAA GAT GAG GAG CTG ACA TTG AAA TAT GGC	482
Val Glu Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly	
65 70 75	
GCC AAG CAT GTG ATC ATG CTC TTT GTC CCT GTG ACT CTC TGC ATG GTG	530
Ala Lys His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val	
80 85 90	
GTG GTC GTG GCT ACC ATT AAG TCA GTC AGC TTT TAT ACC CGG AAG GAT	578
Val Val Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp	
95 100 105 110	
GGG CAG CTA ATC TAT ACC CCA TTC ACA GAA GAT ACC GAG ACT GTG GGC	626

Gly	Gln	Leu	Ile	Tyr	Thr	Pro	Phe	Thr	Glu	Asp	Thr	Glu	Thr	Val	Gly	
				115					120					125		
CAG	AGA	GCC	CTG	CAC	TCA	ATT	CTG	AAT	GCT	GCC	ATC	ATG	ATC	AGT	GTC	674
Gln	Arg	Ala	Leu	His	Ser	Ile	Leu	Asn	Ala	Ala	Ile	Met	Ile	Ser	Val	
			130					135					140			
ATT	GTT	GTC	ATG	ACT	ATC	CTC	CTG	GTG	GTT	CTG	TAT	AAA	TAC	AGG	TGC	722
Ile	Val	Val	Met	Thr	Ile	Leu	Leu	Val	Val	Leu	Tyr	Lys	Tyr	Arg	Cys	
			145				150					155				
TAT	AAG	GTC	ATC	CAT	GCC	TGG	CTT	ATT	ATA	TCA	TCT	CTA	TTG	TTG	CTG	770
Tyr	Lys	Val	Ile	His	Ala	Trp	Leu	Ile	Ile	Ser	Ser	Leu	Leu	Leu	Leu	
	160					165					170					
TTC	TTT	TTT	TCA	TTC	ATT	TAC	TTG	GGG	GAA	GTG	TTT	AAA	ACC	TAT	AAC	818
Phe	Phe	Phe	Ser	Phe	Ile	Tyr	Leu	Gly	Glu	Val	Phe	Lys	Thr	Tyr	Asn	
	175				180				185						190	
GTT	GCT	GTG	GAC	TAC	ATT	ACT	GTT	GCA	CTC	CTG	ATC	TGG	AAT	TTT	GGT	866
Val	Ala	Val	Asp	Tyr	Ile	Thr	Val	Ala	Leu	Leu	Ile	Trp	Asn	Phe	Gly	
				195				200						205		
GTG	GTG	GGA	ATG	ATT	TCC	ATT	CAC	TGG	AAA	GGT	CCA	CTT	CGA	CTC	CAG	914
Val	Val	Gly	Met	Ile	Ser	Ile	His	Trp	Lys	Gly	Pro	Leu	Arg	Leu	Gln	
			210					215					220			
CAG	GCA	TAT	CTC	ATT	ATG	ATT	AGT	GCC	CTC	ATG	GCC	CTG	GTG	TTT	ATC	962
Gln	Ala	Tyr	Leu	Ile	Met	Ile	Ser	Ala	Leu	Met	Ala	Leu	Val	Phe	Ile	
			225				230					235				
AAG	TAC	CTC	CCT	GAA	TGG	ACT	GCG	TGG	CTC	ATC	TTG	GCT	GTG	ATT	TCA	1010
Lys	Tyr	Leu	Pro	Glu	Trp	Thr	Ala	Trp	Leu	Ile	Leu	Ala	Val	Ile	Ser	
	240					245					250					
GTA	TAT	GAT	TTA	GTG	GCT	GTT	TTG	TGT	CCG	AAA	GGT	CCA	CTT	CAT	ATG	1058
Val	Tyr	Asp	Leu	Val	Ala	Val	Leu	Cys	Pro	Lys	Gly	Pro	Leu	His	Met	
	255				260				265						270	
CTG	GTT	GAA	ACA	GCT	CAG	GAG	AGA	AAT	GAA	ACG	CTT	TTT	CCA	GCT	CTC	1106
Leu	Val	Glu	Thr	Ala	Gln	Glu	Arg	Asn	Glu	Thr	Leu	Phe	Pro	Ala	Leu	
				275					280					285		
ATT	TAC	TCC	TCA	ACA	ATG	GTG	TGG	TTG	GTG	AAT	ATG	GCA	GAA	GGA	GAC	1154
Ile	Tyr	Ser	Ser	Thr	Met	Val	Trp	Leu	Val	Asn	Met	Ala	Glu	Gly	Asp	
			290					295					300			
CCG	GAA	GCT	CAA	AGG	AGA	GTA	TCC	AAA	AAT	TCC	AAG	CAT	AAT	GCA	GAA	1202
Pro	Glu	Ala	Gln	Arg	Arg	Val	Ser	Lys	Asn	Ser	Lys	His	Asn	Ala	Glu	
			305				310					315				
AGC	ACA	GAA	AGG	GAG	TCA	CAA	GAC	ACT	GTT	GCA	GAG	AAT	GAT	GAT	GGC	1250
Ser	Thr	Glu	Arg	Glu	Ser	Gln	Asp	Thr	Val	Ala	Glu	Asn	Asp	Asp	Gly	
	320					325					330					
GGG	TTC	AGT	GAG	GAA	TGG	GAA	GCC	CAG	AGG	GAC	AGT	CAT	CTA	GGG	CCT	1298
Gly	Phe	Ser	Glu	Glu	Trp	Glu	Ala	Gln	Arg	Asp	Ser	His	Leu	Gly	Pro	
	335				340					345					350	
CAT	CGC	TCT	ACA	CCT	GAG	TCA	CGA	GCT	GCT	GTC	CAG	GAA	CTT	TCC	AGC	1346
His	Arg	Ser	Thr	Pro	Glu	Ser	Arg	Ala	Ala	Val	Gln	Glu	Leu	Ser	Ser	
				355					360						365	

AGT ATC CTC GCT GGT GAA GAC CCA GAG GAA AGG GGA GTA AAA CTT GGA	1394
Ser Ile Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly	
370 375 380	
TTG GGA GAT TTC ATT TTC TAC AGT GTT CTG GTT GGT AAA GCC TCA GCA	1442
Leu Gly Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala	
385 390 395	
ACA GCC AGT GGA GAC TGG AAC ACA ACC ATA GCC TGT TTC GTA GCC ATA	1490
Thr Ala Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile	
400 405 410	
TTA ATT GGT TTG TGC CTT ACA TTA TTA CTC CTT GCC ATT TTC AAG AAA	1538
Leu Ile Gly Leu Cys Leu Thr Leu Leu Leu Ala Ile Phe Lys Lys	
415 420 425 430	
GCA TTG CCA GCT CTT CCA ATC TCC ATC ACC TTT GGG CTT GTT TTC TAC	1586
Ala Leu Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr	
435 440 445	
TTT GCC ACA GAT TAT CTT GTA CAG CCT TTT ATG GAC CAA TTA GCA TTC	1634
Phe Ala Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe	
450 455 460	
CAT CAA TTT TAT ATC TAGCATATTT GCGGTTAGAA TCCCATGGAT GTTCTTCTT	1689
His Gln Phe Tyr Ile	
465	
TGACTATAAC CAAATCTGGG GAGGACAAAG GTGATTTTCC TGTGTCCACA TCTAACAAAG	1749
TCAAGATTCC CGGCTGGACT TTTGCAGCTT CCTTCCAAGT CTTCTGACC ACCTTGCACT	1809
ATTGGACTTT GGAAGGAGGT GCCTATAGAA AACGATTTTG AACATACTTC ATCGCAGTGG	1869
ACTGTGTCCC TCGGTGCAGA AACTACCAGA TTTGAGGGAC GAGGTCAAGG AGATATGATA	1929
GGCCCGGAAG TTGCTGTGCC CCATCAGCAG CTTGACGCGT GGTCACAGGA CGATTTCACT	1989
GAACTGCGA ACTCTCAGGA CTACCGGTTA CCAAGAGGTT AGGTGAAGTG GTTTAAACCA	2049
AACGGAATC TTCATCTTAA ACTACACGTT GAAAATCAAC CCAATAATTC TGTATTAAC	2109
GAATTCTGAA CTTTTCAGGA GGTACTGTGA GGAAGAGCAG GCACCAGCAG CAGAATGGGG	2169
AATGGAGAGG TGGGCAGGGG TTCCAGCTTC CCTTTGATTT TTTGCTGCAG ACTCATCCTT	2229
TTTAAATGAG ACTTGTTTTT CCCTCTCTTT GAGTCAAGTC AAATATGTAG ATTGCCTTTG	2289
GCAATTCTTC TTCTCAAGCA CTGACACTCA TTACCGTCTG TGATTGCCAT TTCTTCCCAA	2349
GGCCAGTCTG AACCTGAGGT TGCTTTATCC TAAAAGTTTT AACCTCAGGT TCCAAATTCA	2409
GTAAATTTTG GAAACAGTAC AGCTATTTCT CATCAATTCT CTATCATGTT GAAGTCAAAT	2469
TTGGATTTTC CACCAAATTC TGAATTTGTA GACATACTTG TACGCTCACT TGCCCCCAGA	2529
TGCTCTCTCT GTCCTCATTC TTCTCTCCCA CACAAGCAGT CTTTTTCTAC AGCCAGTAAG	2589
GCAGCTCTGT CRTGGTAGCA GATGGTCCCA TTATTCTAGG GTCTTACTCT TTGTATGATG	2649
AAAAGAATGT GTTATGAATC GGTGCTGTCA GCCCTGCTGT CAGACCTTCT TCCACAGCAA	2709

ATGAGATGTA TGCCCAAAGC GGTAGAATTA AAGAAGAGTA AAATGGCTGT TGAAGC

2765

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 467 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Met	Thr	Glu	Leu	Pro	Ala	Pro	Leu	Ser	Tyr	Phe	Gln	Asn	Ala	Gln	Met	1	5	10	15
Ser	Glu	Asp	Asn	His	Leu	Ser	Asn	Thr	Val	Arg	Ser	Gln	Asn	Asp	Asn	20	25	30	
Arg	Glu	Arg	Gln	Glu	His	Asn	Asp	Arg	Arg	Ser	Leu	Gly	His	Pro	Glu	35	40	45	
Pro	Leu	Ser	Asn	Gly	Arg	Pro	Gln	Gly	Asn	Ser	Arg	Gln	Val	Val	Glu	50	55	60	
Gln	Asp	Glu	Glu	Glu	Asp	Glu	Glu	Leu	Thr	Leu	Lys	Tyr	Gly	Ala	Lys	65	70	75	80
His	Val	Ile	Met	Leu	Phe	Val	Pro	Val	Thr	Leu	Cys	Met	Val	Val	Val	85	90	95	
Val	Ala	Thr	Ile	Lys	Ser	Val	Ser	Phe	Tyr	Thr	Arg	Lys	Asp	Gly	Gln	100	105	110	
Leu	Ile	Tyr	Thr	Pro	Phe	Thr	Glu	Asp	Thr	Glu	Thr	Val	Gly	Gln	Arg	115	120	125	
Ala	Leu	His	Ser	Ile	Leu	Asn	Ala	Ala	Ile	Met	Ile	Ser	Val	Ile	Val	130	135	140	
Val	Met	Thr	Ile	Leu	Leu	Val	Val	Leu	Tyr	Lys	Tyr	Arg	Cys	Tyr	Lys	145	150	155	160
Val	Ile	His	Ala	Trp	Leu	Ile	Ile	Ser	Ser	Leu	Leu	Leu	Leu	Phe	Phe	165	170	175	
Phe	Ser	Phe	Ile	Tyr	Leu	Gly	Glu	Val	Phe	Lys	Thr	Tyr	Asn	Val	Ala	180	185	190	
Val	Asp	Tyr	Ile	Thr	Val	Ala	Leu	Leu	Ile	Trp	Asn	Phe	Gly	Val	Val	195	200	205	
Gly	Met	Ile	Ser	Ile	His	Trp	Lys	Gly	Pro	Leu	Arg	Leu	Gln	Gln	Ala	210	215	220	
Tyr	Leu	Ile	Met	Ile	Ser	Ala	Leu	Met	Ala	Leu	Val	Phe	Ile	Lys	Tyr	225	230	235	240
Leu	Pro	Glu	Trp	Thr	Ala	Trp	Leu	Ile	Leu	Ala	Val	Ile	Ser	Val	Tyr	245	250	255	
Asp	Leu	Val	Ala	Val	Leu	Cys	Pro	Lys	Gly	Pro	Leu	His	Met	Leu	Val				

260					265					270					
Glu	Thr	Ala	Gln	Glu	Arg	Asn	Glu	Thr	Leu	Phe	Pro	Ala	Leu	Ile	Tyr
275					280					285					
Ser	Ser	Thr	Met	Val	Trp	Leu	Val	Asn	Met	Ala	Glu	Gly	Asp	Pro	Glu
290					295					300					
Ala	Gln	Arg	Arg	Val	Ser	Lys	Asn	Ser	Lys	His	Asn	Ala	Glu	Ser	Thr
305					310					315					
Glu	Arg	Glu	Ser	Gln	Asp	Thr	Val	Ala	Glu	Asn	Asp	Asp	Gly	Gly	Phe
325					330					335					
Ser	Glu	Glu	Trp	Glu	Ala	Gln	Arg	Asp	Ser	His	Leu	Gly	Pro	His	Arg
340					345					350					
Ser	Thr	Pro	Glu	Ser	Arg	Ala	Ala	Val	Gln	Glu	Leu	Ser	Ser	Ser	Ile
355					360					365					
Leu	Ala	Gly	Glu	Asp	Pro	Glu	Glu	Arg	Gly	Val	Lys	Leu	Gly	Leu	Gly
370					375					380					
Asp	Phe	Ile	Phe	Tyr	Ser	Val	Leu	Val	Gly	Lys	Ala	Ser	Ala	Thr	Ala
385					390					395					
Ser	Gly	Asp	Trp	Asn	Thr	Thr	Ile	Ala	Cys	Phe	Val	Ala	Ile	Leu	Ile
405					410					415					
Gly	Leu	Cys	Leu	Thr	Leu	Leu	Leu	Leu	Ala	Ile	Phe	Lys	Lys	Ala	Leu
420					425					430					
Pro	Ala	Leu	Pro	Ile	Ser	Ile	Thr	Phe	Gly	Leu	Val	Phe	Tyr	Phe	Ala
435					440					445					
Thr	Asp	Tyr	Leu	Val	Gln	Pro	Phe	Met	Asp	Gln	Leu	Ala	Phe	His	Gln
450					455					460					
Phe	Tyr	Ile													
465															